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DB seq length:
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/ Cgn2_6/ptodata/2/pna/US083_COMB.seq:*
/ Cgn2_6/ptodata/2/pna/US083_COMB.seq:*
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44. / cgn2 6/ptodata //pna/US1016 COMB seq:
45. / cgn2 6/ptodata //pna/US1018 COMB seq:
46. / cgn2 6/ptodata //pna/US1018 COMB seq:
47. / cgn2 6/ptodata //pna/US1018 COMB seq:
48. / cgn2 6/ptodata //pna/US1018 COMB seq:
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49. / cgn2 6/ptodata //pna/US1018 COMB seq:
50. / cgn2 6/ptodata //pna/US1018 COMB seq:
51. / cgn2 6/ptodata //pna/US1018 COMB seq:
52. / cgn2 6/ptodata //pna/US1018 COMB seq:
53. / cgn2 6/ptodata //pna/US1016 COMB seq:
54. / cgn2 6/ptodata //pna/US1017 COMB seq:
55. / cgn2 6/ptodata //pna/US1017 COMB seq:
61. / cgn2 6/ptodata //pna/US1017 COMB seq:
62. / cgn2 6/ptodata //pna/US1017 COMB seq:
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67. / cgn2 6/ptodata /
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1

US-10-019-214-1

Sequence 1, Application US/10019214

GENERAL INFORMATION:

APPLICANT: Logan, Susan M.

APPLICANT: Wakarchuk, Warren

APPLICANT: Monteiro, Mario A.

APPLICANT: Honteiro, Mario A.

APPLICANT: Hirateuka, Koji

TITLE OF INVENTION: GLYCOSYLTRANSFERASES OF I

TITLE OF INVENTION: TARGET IN PREVENTION AND TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 12243.24USWO

CURRENT APPLICATION NUMBER: US/10/019,214

CURRENT APPLICATION NUMBER: PCT/CA00/00777

PRIOR APPLICATION NUMBER: 60/140,820
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49 US-08-487-032C-119
8 US-08-487-032C-119
9 US-08-487-032C-119
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13 US-08-993-002A-621
149 US-10-335-977-279
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     RESULT 2
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GENERAL INFORMATION:

APPLICANT: Logan, Susan M.

APPLICANT: Wakarchuk, Warren

APPLICANT: Wakarchuk, Warren

APPLICANT: Wather, Wayne

APPLICANT: Monteiro, Mario A.

APPLICANT: Monteiro, Mario A.

APPLICANT: Monteiro, Mario A.

APPLICANT: Miratewa, Koji

TITLE OF INVENTION: TARGET IN PREVENTION AND TREATMENT OF H. PYLORI

TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 12243.24USWO

CURRENT APPLICATION NUMBER: US/10/019,214

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: ETT/CA00/00777

PRIOR APPLICATION NUMBER: 60/140,820

PRIOR FILING DATE: 1999-06-28

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PATENTIN Ver. 2.1
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                                                                      ATTADAGCTTATAGCGAAGGGGTGGGGACTCAAGGCTATGTGATCACGCCTAAGATTGCC
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Pred. No. 2.6e-199;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 822;
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GENERAL INFORMATION OF SECOTE PRIOR FILING DATE: 400-204 |
APPLICANT: TETSUS ENDO
APPLICANT: TETSUS ENDO
APPLICANT: KASUNINKO TABATA
APPLICANT: AKIO OZAKI
ITITE OF INVENTION: GLYCOSYLTRANSFERASE AND DNA ENCODING THE
FILE REFERENCE: 2139.18
CURRENT APPLICATION NUMBER: US/10/218.381
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: PCT/JP99/00321
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: PCT/JP99/00321
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: JP 10-023389
PRIOR FILING DATE: 1998-02-04
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 819
TYPE: DNA
GRGANISM: Helicobacter pylori
US-10-218-381-2
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Best Local Sim
Matches 790;
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                                                                    ATCTGTATTTTAGAAGACGATATAACCTTGAAAGAGGATTTTAAAGAGGGCTTGGATTTT
                                                                                                              CTTGGGTGCTATGCGAGCCATTATTCCTTGTGGGAAAAATGCATAGAACTCAATGAAGCG
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ilarity 96.5%;
Conservative
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RESULT 4
US-08-761-066-185
             APPLICATION NUMBER:

PILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PILING DATE:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: GTN-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-7400

TELEFAX: (617)227-791

INFORMATION FOR SEQ ID NO: 185:

SEQUENCE CHARACTERISTICS:

LENGTH: 822 base pairs

TYPE: nucleic acid

STRANDENESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO
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GENERAL INFORMATION:
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STREET: 60 State Stree
CITY: BOSCON
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS
COMPUTER: SYSTEM:
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DOUGLAS SMITH ET AL
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI AND
TITLE OF INVENTION: THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 714
CORRESPONDENCE ADDRESS: LAHIVE & COCKFIELD
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; ORGANISM: Helicobacter [
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1...822
US-08-761-066-185
RESULT 5
US-08-993-002A-3963
: Sequence 3963, Application US/08993002A
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
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nilarity 94.9%;
Conservative
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Pred. No. 2.3e-194;
0; Mismatches 42;
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Best Local Sim
Matches 780;
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INFORMATION FOR SEQ ID NO: 3963:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: ofrcular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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MEDIUM TYPE: CD/ROM 1509660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,002A
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TITLE OF INVENTION: RELATING TO
TITLE OF INVENTION: DIAGNOSTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: misc_feature LOCATION: 1...822
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ORIGINAL SOURCE:
ORGANISM: Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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STREET: 28
CITY: Bost
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Similarity 94.9%;
80; Conservative
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                      CACCCTTATTTCATCACGCAAAATATCAAAGACATGGGGATTGCAACCAGTCTCATCAGT
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RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pylori
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 754.8; DB 13;
Pred. No. 2.3e-194;
0; Mismatches 42;
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US-10-335-977-3963
US-10-335-977-3963
; Sequence 3963, Application US/10335977
; GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
PRINCIPLE OF AND THERAPEUTICS
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 INFORMATION FOR SEQ ID NO: 3963:
SEQUENCE CHARACTERISTICS:
LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM IS09660

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
PRIOR MAME: MANGER 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANGER 507
REGISTRATION NUMBER: 36,207
REGISTRATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-740
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CITY: Boston
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NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...822
SEQUENCE DESCRIPTION: SEQ ID NO: 3963:
US-10-335-977-3963
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Best Local S
Matches 780
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                 GAACTCCATTTTAAATATTTGAAATATTGGCAGTTTGTATAA 822
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                                                                                                                                                                                                                                                                                          ATTAAAGCTTATAGCGAAGGGGTGGGGACTCAAGGCTATGTGATCACGCCCTAAGATTGCC
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                                                                 CAAATCTCTACGATAGCGCGAAAAGAAGAACCCTATAGCCCTAAAAATCGCTCTAATGAGA
                                                                                                                                 ACTITIATCCATGGCGTGAAAAATCTGGTGTTACAACCTTTTGTGATCGCTGATGATGAG
                                                                                                                                                       ACTITIATCCATGGCGTGAAAAATCTGGTGTTACAACCTTTTGTGATGATGATGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.8%; Score 754.8; DB 49 ilarity 94.9%; Pred. No. 2.3e-194; Conservative 0; Mismatches 42;
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GENERAL INFORMATION:
APPLICANT: Douglas Smith
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
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US-08-621-425-478
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INFORMATION FOR SEQ ID NO: 478:
SEQUENCE CHARACTERISTICS:
LENGTH: 9382 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 91.6%; Score 753.2; DB 10; Best Local Similarity 94.8%; Pred. No. 1.6e-193; Matches 779; Conservative 0; Mismatches 43;
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CITY: BOSTON
STATE: Massachusetts
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: 8mm cartridge tape
COMPUTER: SPARC station LX
OPERATING SYSTEM: SUNOS4
SOFTMARE: tar
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,425
FILING DATE: 25-MARCH-1996
FILING DATE: 17-NOV-1995
FILING DATE: 17-NOV-1995
PRIOR APPLICATION NUMBER: 08/487,032
APPLICATION NUMBER: 08/487,032
FILING DATE: 07-MATION:
NAME: MANDERS: 36,207
REFERENCE/DOCKET NUMBER: CTN-0010
TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter p
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...9382
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFLELD
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RESULT 8
US-08-993-002A-3964
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GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                  STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
COMPUTER: CD/ROM IS09660
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.
SOFTWARE: UNIX
ATTORNEY/AGENT INFORMATION:
NAME: MANDErsas, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                  PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter py
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..837
US-08-993-002A-3964
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Best Local Similarity 94.7
Matches 776; Conservative
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                       CAAATCTCTACGATAGCGCGAAAAAGAAGAACCCTATAGCCCTAAAAATCGCTCTAATGAGA
                                                                          ACTTTTATCCATGGCGTGAAAAATCTGGTGTTACAACCTTTTGTGATCGCTGATGATGAG
                                                                                          ACTTTTATCCATGGCGTGAAAAATCTGGTGTTACAACCTTTTGTGATGATGATGAG
                                                                                                                                  AAAGTTTTTTTGAAACACAGCCGAAAATGGGTTGTTCCTGTGGATACGATAATGGACGCT
                                                                                                                                                  AAAGTTTTTTTGAAATGCAGCCGAAAATGGGTTGTTCCTGTGGATACGATAATGGACGCT
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                                                                                                                                                                                                                                                                                                                                                             ATCTGTATTTTAGAAGACGATATAACCTTGAAAGAGGATTTTAAAAGAGGGCTTGGATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.3%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 750.2; DB 13
Pred. No. 4.2e-193;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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RESULT 9
US-10-335-977-3964
US-10-335-977-3964
; Sequence 3964, Application US/10335977
; GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...837
SEQUENCE DESCRIPTION: SEQ ID NO: 3964:
US-10-335-977-3964
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC COMPARELD1e
OPERATING SYSTEM: WINDOWS NT 4.0
SOPTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION UNDSER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MANDEAGOULES, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-7400
TELEPAX: (617)742-4214
INFORMATION POR SEQ ID NO: 3964:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
  181
                                                                                                             121
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                                                                                                                                                                                                                                                                                                            TIGCGIGITITITGCCATITCTITAAAICAAAAAGIGIGGGAIACATIIGGITITAGITITIT
CACCCTTATTTCATCACGCAAAACATCAAAGACATGGGGATTACAACCAATCTCATCAGT
                                                                                                          GATGCGATTTATTCTAAAACTTTTGAAGGCGGGTTGCACCCCTTAGTGAAAAAGCATTTA 180
                                                                                                                                                                                                                     GAACTCCATTTTAAATTTTTGAAATGGTGGCAGTTTGTA
                                                      GATGCGATTTATTCCAAGACTTTTGAAGGCGGGTTGCACCCCCTAGTTAAAAAAGCATTTA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                    ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACTCCATTTTAAATATTTGAAATATTTGGCAGTTTTGTA
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              91.3%;
94.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 750.2; DB 49; Pred. No. 4.2e-193;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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US-08-487-032A-119
; Sequence 119, Application US/08487032A
; GENERAL INFORMATION:
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              SOFTWARE: Patentin Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,032A
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001
TELECOMMUNICATION TUMBER: GTN-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: RELATI
TITLE OF INVENTION: DIAGNO
TITLE OF INVENTION: DIAGNO
NUMBER OF SEQUENCES: 880
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCK
                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 60 SI
                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTAAAGCTTATAGCCATGGGGGGGGGGCGCAAGGCTATGTGATCACGCCCAAGATTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                              Version #1.25
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558 600

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438 480 360

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RESULT 11
US-08-487-032C-119
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 119, Application US/08487032C

GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH
APPLICANT: DOUGLAS SMITH
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: misc_feature
LOCATION: 1...285
COTHER INFORMATION: /note= "influenzae type B
OTHER INFORMATION: lipooligosaccharide"
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release +ACM-1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/487,032C
APPLICATION UNMBER: UJ/08/487,032C
FILING DATE: 07-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION UNMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 941
CORRESPONDENCE ADDRESSE: LAHIVE +ACY-
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 32.0%; al Similarity 95.4%; 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGATTTTAAAGAGAGGCTTGGATTTTTTAGAAAAACACATCCAAGAGTTAGGCTATATC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTTTGATGCATTTATTGTATGATGCCAGCGTGAAAAGTGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCTTGATGCATTTATTGTATGATGCCAGTGTAAAAAGTGAGCC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGATTTTANAGAGGGCTTGGATTTTTTAGANAAACACATCCAAGAGTTAGGCTATGCG 240
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                                                                                                                                                                                                                                                                                         STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119:
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                                                                                                                                                                                                                                                                                                                                                       COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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US-08-561-469A-119
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                                                                                                                                                                                                                                                                                     Sequence 119, Applica GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 271; Conserv
                       ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pateentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/561,469A
FILLNG DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       STREET: 00
STREET: 00
TTY: Boston
                                                                                                                                                                                                                             COUNTRY: USA
        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc+AF8-feature
LOCATION: 1...285
OTHER INFORMATION: /note+AD0- +ACI-influenzae type
lipooligosaccharide+ACI-
SEQUENCE DESCRIPTION: SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 CGCTTGATGCATTTATTGTATGATGCCAGTGTAAAAAAGTGAGCC 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CAAAATGCATAGAGCTCAATGAAGCGATCTGTATTTTAGAAGACGATATAACCTTGAAA
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                                                                                                                                                                                                                                                     Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08561469A
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                                                                                                                                                                                                                                                                                                                                                                          NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
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        US 08/487,032
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Pred. No. 1.1e-60;
0; Mismatches 13;
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US-08-993-002A-9621
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                                                                                                                                                                                                                                                                           Sequence 9621, Application US/08993002A

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.0
Best Local Similarity 95.4
Matches 271; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: MANDERS AMPE E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1...285
OTHER INFORMATION: /note= "influenzae type
OTHER INFORMATION: lipooligosaccharide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1...285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
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                                                                                                                     02109-1875
APPLICATION DATA:
                                                                                                                                                                                 Boston
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                                                                                                                                                            Massachusetts
                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.0%; Score 263.2; DB 9
95.4%; Pred. No. 1.1e-60;
sive 0; Mismatches 13
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RESULT 14
US-10-335-977-9621
; Sequence 9621, Application US/1033597.
; GENERAL INFORMATION:
; GENERAL INFORMATION:
ITTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION INVENTION TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
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SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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Best Local Similarity
Matches 271; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DN)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helico
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: 1...285
COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT
                                                                                                              NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                             454 CGCTTGATGCATTTATTGTATGATGCCAGTGTAAAAAAGTGAGCC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CAAAAATGCATAGAGCTCAATGAAGCGATCTGTATTTTAGAAGACGATATAACCTTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 GAAAAATGCATAGAACTCAATGAAGCGATCTGTATTTTAGAAGACGATATAACCTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGCGAAATTTATGAGCTTGGGGGAGCTTGGGTGCTATGCGAGCCATTATTCGTTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGATTTTAAAGAGGGCTTGGATTTTTTAGAAAAACACATCCAAGAGTTAGGCTATGCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 263.2; DB 13; Pred. No. 1.1e-60; 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTN-018
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RESULT 15
US-08-993-002A-2792
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LOCATION: (B) LOCATION 1...285
SEQUENCE DESCRIPTION: SEQ ID NO: 9621:
US-10-335-977-9621
                                                                                                                                                                                Sequence 2792, Application US/08993002A

GENERAL INFORMATION:

APPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES

TITLE OF INVENTION: RELATING TO HELICOBACTER PYLORI FOR

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 32.0%;
Best Local Similarity 95.4%;
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9621:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
COMPUTER READABLE FORM:
                                                                                                                        NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
               STREET: 28 State
CITY: Boston
STATE: Massachus
COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
PILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN
TELECOMMUNICATION IMFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                             454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAAAATGCATAGAACTCAATGAAGCGATCTGTATTTTAGAAGAGACGATATAACCTTGAAA 393
                                                                                                                                                                                                                                                                                                                                                                                                       CGTTTGATGCATTTATTGTATGATGCCAGCGTGAAAAGTGAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCTTGATGCATTTATTGTATGATGCCAGTGTAAAAAGTGAGCC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGATTTTAAAGAGGGCTTGGATTTTTTAGAAAAACACATCCAAGAGTTAGGCTATATC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAAAATGCATAGAGCTCAATGAAGCGATCTGTATTTTAGAAGACGATATAACCTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGGGATTGCAACCAGTCTCATCAGTGAGGTTTCTAAGTTTTATTACGCTTTAAAATAC 60
                                                              Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Helicobacter pylori
                                                                                                      28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 263.2; DB 49;
Pred. No. 1.1e-60;
0; Mismatches 13;
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TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 279.
SEQUENCE CHARACTERISTICS:
LENGTH: 846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 450; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MANDATES ANY E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DY HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: CD/ROM 101.
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT
COFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 1...846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
                                                                                                                                                                                                                                                                                302
                                                                                                                                                                                                                                                                                                                    299 AGCTTGGGTGCTATGCGAGTCATTATTCCTTGTGGGAAAAATGCATAGAACTCAATGAAG
                                                                                                                                                                                                                                                                                                                                                               242 GCGCGTTAAAAAATTTCTTTTACGCGCTCAAGCATTGCGGGAAGAGGGATGGGGTTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 ACCCTTCTTTTATGGTTGAAGATTTATTGGCTTTTTGTAAAAATAAAAAAACACCCCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 ACCCTTATTTCATCACGCAAAAACATCAAAGACATGGG----GATTACAACCAATCTCATCA 238
                                                                                                                                                                                              362
                                                                                                                                                                                                                                 359 CGATCTGTATTTTAGAAGACGATATAACCTTGAAAGAGGATTTTAAAAGAGGGCTTGGATT
                                                                                                                                                                                                                                                                                                                                                                                                           239 GIGAGGITTCIAAGITITATTACGCITTAAAATACCATGCGAAGITTATGAGCITGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 ATGCGATCTATTCTAAAATCTCTCCCACTCAATTACACCCCTTGATTTTAGAGCATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 ATGCGATTTATTCTAAAACTTTTGAAGGCGGGTTGCACCCCTTAGTGAAAAAGCATTTAC
                          482 TGGCTANACANAAGACTCCAGTTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CTCATATAACCCCCCTTTTAGAGAGCCTTAAACTTCAAGGGATCTCTTATGAAATTTTTG
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                                                                CCAGTGTAAAAAGTGAGCCATTGAGCCATAAAAACCACGAGATACAAGAGCGTGTGGGGA 538
                                                                                                                                 TTTTAGAAAAACACATCCAAGAGITAGGCTATATCCGCTTGATGCATTTATTGTATGATG 478
                                                                                                                                                                                              AGCTTGGGTGCTATGCGAGCCATTATTCGTTGTGGCAAAAAATGCATAGAGCTCAATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGTGTTTTTATTCATTTAAGCCCCCAAAACCTGTAAAAATTTTTCTTTAAAAAGAAA 61
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ilarity 59.5%;
Conservative (
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Pred. No. 6e-50;
0; Mismatches 276;
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Length 846;

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AAGGGGTTTCTC 517

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